Molecular typization of Arthroderma benhamiae, a zoonotic agent of epidemic dermatophytosis in Central Europe

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Objectives

The aim of this study was to find informative molecular markers to evaluate population structure of dermatophyte species Arthroderma benhamiae in the studied area. One of the main issues was to determine whether the current outbreak of dermatophytosis caused by A. benhamiae in Central Europe is caused by a new more virulent genotype which is with the high success rate transmitted to humans or whether other causes must be considered (e.g. high prevalence of the pathogen in animal husbandry).

Methods A total number of 262 A. benhamiae strains associated with cases of human and animal dermatophytosis from the Czech Republic (CZ), Belgium, UK, Germany, Italy, Japan and USA were used for analysis. Ten microsatellite markers were developed and used for typization of A. benhamiae strains together with sequence analysis of ITS region rDNA and glyceraldehyde-phosphate dehydrogenase gene. Bayesian inference analysis and distance methods were applied on the datasets to reveal the genetic variation of A. benhamiae population. PCR-based determination of mating idiomorphs was also performed in all strains. Results The sequence analysis based on two genes revealed presence of five genotypes. Most common genotype (n = 195, 74.4%) was characterized by yellow colony reverse on MEA agar with the exception of isolates from dogs in North America which showed different phenotype. Only MAT1-1 idiomorph was amplified in isolates of this genotype from Europe and low variability in microsatellites data was recorded. In contrast, the isolates of this genotype from North America were highly variable by microsatellite data and isolates of both mating type genes were revealed. The second most common genotype (n = 47, 17.9%) was characterized by dominant red (mating type MAT2) or brown (MAT1) colony reverse on MEA agar. The third genotype (n = 16), closely related to second genotype, included all strains from Japan and some from the CZ and Belgium and was characterized by both red and yellow colony reverse and MAT1-1 idiomorph. The remaining two genotypes were each represented by only two isolates from the CZ.

Conclusion A. benhamiae is a new emerging pathogen in the CZ and some other countries in Central and Western Europe region. According to recent studies this species is the most important zoophilic dermatophyte in the CZ causing almost 23% of tinea corporis (median age of patients – 10 years, females - 70%) and 29% of tinea capitis infections. The majority of infections are transmitted from guinea pigs and other rodents. It is probable that the most common genotype of A. benhamiae responsible for the outbreak of infections in the Central Europe (agent of 79.7% of human infections in the CZ) spread clonally. This hypothesis is also supported by uniform phenotype and mating type in European strains. The american strains of the same genotype (can be separated by microsatellite data) however showed different phenotype and presence of both mating type genes indicating sexual reproduction. Other genotypes contribute only marginally on the outbreak.